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EXAMINER	
HIBBERT, CATHERINE S	

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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/705,874	WANG ET AL.	
	Examiner	Art Unit	
	CATHERINE HIBBERT	1636	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE *3* MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *30 June 2008*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *90 and 92-110* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *90 and 92-110* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Please note that the Examiner for this Application has changed. Applicants Amendments to the Claims filed 30 June 2008 have been received and entered. Claims 1-89 and 91 are cancelled. Claims 90, 92-96, 99 and 104-108 have been amended. Claims 90 and 92-110 are pending and under examination.

Response to Applicants Arguments/Amendments

Claim Rejections - 35 USC § 112

The rejection of Claims 92-96 and 104-108 for indefiniteness is WITHDRAWN based on Applicants amendments to the claims.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

Claims 90, 92-95, 97-107 and 109-110 STAND rejected under 35 U.S.C. 102(a) as being anticipated by Bensimon et al (US Patent App. Pub. No. 2002/0048767, 4/25/2002, entire document, of record) for reasons of record and below.

Applicants arguments have been fully considered but are not persuasive.

It is noted that claims 90 and 99 recite the phrases "pieces within a plurality of windows of fixed size of the genome" and “each window comprises a plurality of pieces

and the pieces within a window are genomically clustered". It is noted that the terms “pieces” and “window” have not been given limiting definitions in the specification, especially regarding the size of the “pieces” and ”windows”. Therefore, the terms and phrases will be given the broadest reasonable interpretation.

Claims 90 and 99 recite the phrase "windows of fixed size". It is noted that the instant disclosure does not specify a specific size or a limiting definition of the term "fixed size". The term "fixed size" can be given the broadest reasonable interpretation regarding how the size of the window would be “fixed” or designated. In addition, as the claim is written it does not require that one window of “fixed size” is the same “fixed size” of another window in the recited plurality of windows. Applicants amendments to Claims 90 and 99 which recites "each of said windows having the fixed size" is not remedial in this regard because the limitation, as written, still does not require that one window of “fixed size” is the same “fixed size” of another window in the recited plurality of windows. Bensimon et al teach methods of detecting changes in a genome including deletion or translocation, or changes in number of copies of certain sequences and teach methods which allow genes to be located and mapped rapidly (see paragraph 0005).

Bensimon et al in particular uses a method known as molecular combing to anchor and stretch DNA molecules by the end to produce DNA molecules aligned in a parallel manner. Bensimon et al teach that the DNA can be of any size, and includes genomic DNA extracted from human cells (see paragraph 0036, for example), which meets the limitation of a genome of a test eukaryotic cell. Bensimon et al teach that the

method comprises attaching and combing a DNA B to a combing surface, reacting the DNA B combing product with one or more labeled probes bound to a DNA A. Bensimon et al teach that this method can determine information about the position of the probes on the sample DNA B, the distance between the probes and the size of the probes in order to determine the presence, location and quantity of sequences of DNA A (see paragraphs 0043-0047).

Bensimon et al teach a method to search for genes involved in particular pathologies in an affected target population using DNA. Bensimon et al teach that known genetic markers and probability analysis are used to narrow genetic locations on one or more chromosomes. Several human DNA library clones that contain relevant genetic markers are obtained. Bensimon et al teach that a region of interest can be precisely mapped using clones of decreasing size. Bensimon et al teach that any of several known molecular techniques can be used to assign a coding sequence to one or more of the clones selected in the preceding steps (see paragraphs 0027-0031 and 0152, for example), which meets the limitation of identifying pieces of the genome of a test eukaryotic cell by determining nucleotide sequence of said pieces. Absent evidence to the contrary, pieces of DNA sequence in a DNA library clone would be genomically clustered. Bensimon et al incorporate molecular combing techniques in which the combed DNA is denatured and hybridized with fluorescent probe fragments. Bensimon et al teach that the size of the hybridized probe fragments can be precisely determined by measurement of the lengths of the fluorescent fragments (see paragraphs 0037-0040). Bensimon et al teach that probes are polynucleotide sequences containing at

least 20 nucleotides, a genomic DNA fragment and a contig. Bensimon et al teach that a contig is a set of probes which are contiguous, or overlap and cover the region of interest, or comprises several separate probes. Bensimon et al teach an embodiment in which the length of the probes is between 5 kb -50 kb (see paragraph 0052 and 0054, for example). Bensimon et al teach that this method will provide information about the position of the probes, the distance between the probes and the size of the probes that are hybridized to the sample DNA. The denatured combed genomic DNA sequence to which a probe hybridizes, meets the limitation of a piece of a genome. Bensimon et al disclose embodiments in which the probe contigs are contiguous, or overlap to cover the region of interest or are several separate probes for the region of interest, which meets the limitation of multiple pieces of a genome within a window. Bensimon et al teach that determination of total sum of the sizes of the probes make it possible to quantify the number of hybridized probes to deduce the quantity of the genes or sequence of the specific test DNA A (see paragraph 0044-0047).

Bensimon et al teach an embodiment in which the method is practiced to determine the position of potential genome break points associated with a genetic pathology where the position of a genomic probe of known size is determined in the region of a desired gene (see paragraph 0059, for example). Since “windows of a fixed size” can be given the broadest reasonable interpretation, a genomic window that contains a sequence that can hybridize to a probe of a known size would meet the limitation of a window of fixed size. Bensimon et al also teach that it is important to have a large number of hybridized probes, and several types of control and target

probes (see paragraph 0102, for example). Bensimon et al teach that the data can be expressed in a histogram so that the number of clones having defined probe length is evaluated (see paragraph 0068, for example). Bensimon et al exemplify simultaneous hybridizations of two cosmids on human genomic DNA separated by a gap of several tens of kb and found that it was possible to measure about eighty coupled signals (see Example 1 paragraph 0311, for example). Therefore, Bensimon et al contemplate enumerating pieces within a plurality of windows of fixed size wherein each window comprises a plurality of pieces and the pieces within a window are genomically clustered.

Bensimon et al teach that if a sufficient density of combed DNA molecules is available, detection of relatively small sequence deletions is possible. Bensimon et al teach that it is particularly advantageous to use at least about ten copies of the genome in the combing method (see paragraphs 0100 and 0245, for example). Therefore, Bensimon et al also contemplate performing a plurality of comparisons for the plurality of windows. Bensimon et al teach that the break points consist of points in the genetic sequence whose surroundings change over several kilobases in a diseased subject when compared to a healthy subject (see paragraph 0059, for example). Bensimon et al present histograms illustrating data from an abnormal allele after subtraction of data obtained from a normal allele (see paragraph 0170 for example), which meets the limitation of a method step of comparison of a first number of pieces counted within windows for a genome of a test eukaryotic cell compared to a second number of pieces counted within the windows for a genome of a reference (i.e. normal) cell where a

difference indicates a karyotypic difference between the test and the reference genome of the eukaryotic cell (claim 90).

Bensimon et al teach that this method can be used to determine change in gene copy number which can be used to detect the absence of a portion of the genome(see paragraphs 0112 and 0099, for example), which meets the limitation of a method of determining changes in copy number of portions of a genome of a test eukaryotic cell, wherein a first number of pieces counted within windows for a genome of a test eukaryotic cell compared to a second number of pieces counted within the windows for a genome of a reference (i.e. normal) cell where a difference indicates a changes in copy number of a portion of the genome between the test and the reference genome of the eukaryotic cell (claim 99). Bensimon et al exemplify hybridization of probes over a distance of about 120 kb (see paragraph 0311, for example), which meet the limitation of a method wherein the pieces within the windows map to within 200 kb (claims 93 and 105). Bensimon et al teach embodiments in which the lengths of the probes used in the method are between 5 kb -50 kb but may also consist of the entire combed genome (see paragraph 0054, for example). Bensimon et al teach that it is possible to detect genomic deletions of the size of a cosmid clone (30-50kb) or greater. Therefore Bensimon et al meet the limitation of a method wherein the pieces within the windows map to within 40 kb (claims 92 and 104). Bensimon et al teach embodiments in which the lengths of the probes used in the method may also consist of the entire combed genome (see paragraph 0054, for example), which absent evidence to the contrary

meets the limitation of a method wherein the pieces within the windows map to within 600kb (claims 94 and 106) or to within 4Mb (claims 95 and 107).

Bensimon et al contemplate detection of genomic deletions and insertions of substantial portions of chromosomes (see paragraphs 0014, 0071 and 0079-0083), which meets the limitations of a method wherein the change in copy number is due to an interstitial deletion (claim 103) or loss of a chromosomal arm (claim 101). Bensimon et al contemplate detection of duplication of several copies of all or part of genomic region (see paragraphs 0084), which meets the limitations of a method wherein the change in copy number is due to an interstitial amplification (claim 102). Bensimon et al contemplate detection of major duplications such as those of the trisomy disorders where the sequence represents the whole of a chromosome (see paragraph 0084 and 0006, for example), which meets the limitations of a method wherein the change in copy number is due to gain of a whole chromosome (claim 100).

Bensimon et al exemplify a combing method for human genomic DNA comprising hybridization of two cosmids over a distance of about 120 Kb (see paragraph 0311, for example). Absent evidence to the contrary 120 kb represents less than 15% of the human genome. Therefore, Bensimon et al meet the limitation of a method for karyotyping a eukaryotic genome wherein pieces representing less than 15% of the human genome of the eukaryotic cell are enumerated in the step of enumerating (claim 98). Bensimon et al also meet the limitation of a method for detecting changes in copy number of portions of a genome of a test eukaryotic cell wherein pieces representing

less than 15% of the human genome of the eukaryotic cell are enumerated in the step of enumerating (claim 110).

Bensimon et al teach embodiments of calculation of changes in copy number relative to a control sequence. Bensimon et al teach that a ratio of control to test of close to 1.5 will indicate a trisomic genotype (see paragraphs 0089-0090 and 0093 in particular), which meets the limitation of a method comprising the step of identifying aneuploidy if the pieces of one or more autosomes are determined to be present in the test eukaryotic cell relative to the reference eukaryotic cell at a ratio of 1.5 or greater or less than 0.7 (claims 97 and 109).

Applicants response is to traverse the rejection of Claims 90, 92-95, 97-107, and 109-110 under 35 U.S.C. § 102(a), as anticipated by Bensimon et al. Applicants argue that Bensimon's teachings are substantially different from the claimed methods and that “even giving the claim terms the broadest possible constructions, Bensimon does not fall within them”. Applicants argue that Bensimon does not teach any of the three steps of the independent Claims 90 and 99 and therefore also does not teach the dependent claims. Specifically, Applicant argues that Bensimon fails to teach the method step of identifying pieces of the genome of the test eukaryotic cell by determining nucleotide sequence of said pieces”. Applicant states that Bensimon does not teach this step in paragraphs 0027-0031 and 0152, as stated in the previous Office Action, nor “in any other passage applicants have located”. Applicants further state that:

> Paragraphs 0027-0031 purport to describe the state of the art research methods for identifying genomic sequences responsible for diseases. See paragraphs 26 and 27, in particular. Paragraph 28 simply discloses collection of samples from affected individuals. Paragraph 29 describes linkage analysis. Paragraph 30 describes physical mapping and cloning of a region determined to be involved in the disease. Paragraph 31 teaches the use of cDNA libraries, CpG islands, preservation of interspecific sequences to assign a coding sequence to one or more clones. Paragraph 0152 teaches the location or detection of products capable of reacting with combed DNA. Such products are proteins. Their binding sites can be determined. In none of these paragraphs does Bensimon teach nucleotide sequence determination of pieces of a genome of a test eukaryotic cell, as recited in step 1.

Applicants further argue that "The failure of Bensimon to teach the very first step of the method underscores the fact that other parts of the reference that the U.S. Patent and Trademark Office alleges teach parts of the claimed method are plucked out of their context and applied willy-nilly to the claimed methods. The random extraction, rearrangement, and stitching together of isolated words and sentences does not constitute a teaching of the invention". In addition, Applicants state that "the failure to teach step 1 is sufficient to prevent Bensimon from constituting an anticipatory reference". In addition, Applicants argue that Bensimon also does not teach step 2 of the base claims 90 and 99 because Applicants argue that "Bensimon does not teach enumerating pieces of the genome of a test eukaryotic cell within a plurality of windows of a fixed size, each of said windows having the fixed size, wherein each window comprises a plurality of pieces and the pieces within a window are genomically clustered". Applicant notes that:

> The Office Action points to probes which hybridize to genomic DNA as being "pieces of a genome." Page 6, line 3. But the probes are not pieces of the genome of a test eukaryotic cell, as the claims require. Thus while Bensimon may determine the sum of sizes of probes, Bensimon does not

> "enumerate the pieces [of the genome of the test eukaryotic cell] within a plurality of windows ...." The plain meaning of enumerating is counting; determining the sum of sizes of objects is not the same as counting the number of such objects.

Additionally, Applicants argue that Bensimon does not teach step 3 of claims 90 or 99, reasoning that "if Bensimon does not teach identifying or enumerating [counting] pieces of the genome of a test eukaryotic cell, perforce he does not teach comparing the number of pieces enumerated within a plurality of windows from the test cell to the same for a reference cell.

Applicants arguments have been fully considered but are not found persuasive for reasons of record and presented herein. Specifically, Applicants argument that Bensimon et al fails to teach "enumerating" because the "plain meaning of enumerating is counting" and that "determining the sum of sizes of objects is not the same as counting the number of objects" is not persuasive because the term "enumerating" can be read as "counting" or "listing" and clearly in order to determine the sum of sizes of objects both "counting" and "listing" would inherently be employed. In addition, although the "probes" are not themselves the pieces of the genome, the probes are the identifiers of the pieces of the genome that are being analyzed.

In addition, Bensimon et al teach that any of several known molecular techniques can be used to assign a coding sequence to one or more of the clones selected in the preceding steps (see paragraphs 0027-0031 and 0152, for example), which meets the limitation of identifying pieces of the genome of a test eukaryotic cell by determining nucleotide sequence of said pieces.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

Claims 96 and 108 STAND rejected under 35 U.S.C. 103(a) as being unpatentable over Bensimon et al (US Patent App. Pub. No. 2002/0048767, 4/25/2002) in view of Kong et al (US Patent No. 5,200,336, 4/6/1993, of record) for reasons of record and below.

Applicants arguments have been fully considered but are not persuasive.

Applicants claim a method of karyotyping a genome of a test eukaryotic cell or determining changes in copy number of portions of the genome, wherein the pieces of the genome are defined by the presence of a BcgI restriction endonuclease recognition site flanked by 12 nucleotides at either end.

The teaching of Bensimon et al is detailed in the rejection above. In particular, Bensimon et al teach that known genetic markers and probability analysis are used to narrow genetic locations on one or more chromosomes. Several human DNA library clones are obtained and a number of clones that contain relevant genetic markers are obtained. Bensimon et al teach that a region of interest can be precisely mapped using clones of decreasing size (see paragraphs 0027-0031 and 0152, for example).

Bensimon et al teach an embodiment of the method comprising a step of mapping restriction fragments of combed DNA instead of mapping subclones in order to produce a physical map of the restriction fragments with sufficient accuracy to allow a reconstitution of a final sequence. Bensimon et al teach that the applicability of this technique is dependent on adequate size of the main genomic fragments and on subsequent subcloning of the DNA into small size vectors after additional enzymatic restriction for sequencing (see paragraphs 0340-0342, in particular). Bensimon et al does not specifically teach a method where pieces of the genome are defined by the presence of a BcgI restriction endonuclease recognition site flanked by 12 nucleotides at either end.

Kong et al teach a Type II restriction endonuclease known as BcgI. Kong et al teach the recognition sequence of BcgI:

5'-$(N)_{10}$CGA$(N)_6$TGC$(N)_{12}$-3'

3'-$(N)_{12}$GCT$(N)_6$ACG$(N)_{10}$-5'

and teaches that it enzymatically cleaves at both ends outside of its recognition sequence.

Kong et al teach that BcgI digestion of DNA produces a 34 base pair fragment (see abstract and column 1, lines 60-65 and column 6, lines 16-20, in particular). Since the recognition sequence is centrally located and has 10-12 variable nucleotides on either side, presence of the recognition sequence would define a genomic sequence piece which is flanked by 12 nucleotides on either end. Kong et al teach that BcgI can be used in a method of mapping DNA by forming a DNA library from fragments that

result from digesting the DNA with BcgI, separating the individual clones and using them as probes for target DNA. Kong et al teach that the probes would contain sufficiently unique DNA to allow identification of large regions of DNA from which they were obtained. Kong et al teach that when BcgI is used, the individual cloned 32 base pair fragments uniquely identify and tag a larger DNA sequence. Kong et al teach that the overlap of two larger fragments could be readily established (see column 7, lines 19-40, in particular).

It would be obvious to the skilled artisan at the time the invention was made to modify the method taught by Bensimon et al and define a piece of the eukaryotic genome with a BcgI recognition site when preparing human DNA library clones for mapping and subsequent detection of gene copy number because Bensimon et al teach steps of mapping restriction segments and Kong et al teach that BcgI can be used to create probes with unique identifiable DNA. The motivation to use BcgI as the enzyme to create restriction fragments for cloning and mapping is the expected benefit of being able to produce a DNA library with unique DNA that would hybridize specifically to unique positions in chromosomal DNA as taught by Kong et al (see column 9, lines 20-25, for example) and Kong et al teach that BcgI would be particularly useful in mapping human chromosomal DNA (see column 7, lines 19-40, in particular). There is a reasonable expectation of success to define pieces of genomic DNA by the presence of BcgI in a method for determining karyotypic differences or changes in copy number of portions of the genome because Kong et al used BcgI to enzymatically digest chromosomal DNA. Given the teachings of the prior art and the level of skill of the

ordinary skilled artisan at the time the invention was made, it must be considered that said ordinary skilled artisan would have had a reasonable expectation of success in practicing the claimed invention. Therefore, Bensimon et al in view of Kong et al render obvious a method of karyotyping a genome of a test eukaryotic cell or determining changes in copy number of portions of the genome, wherein the portion of the genome are defined by the presence of a BcgI restriction endonuclease recognition site flanked by 12 nucleotides at either end (claims 96 and 108).

Applicants response is to traverse the rejection of Claims 96 and 108 under 35 U.S.C. § 103(a) as obvious over Bensimon (supra) in view of Kong (US 5200336). Applicants argue that Claims 96 and 108 are dependent from claims 90 and 99, respectively, and therefore for "at least the reasons detailed above, Bensimon does not teach the methods of claims 96 and 108". In addition, Applicants argue that "Kong's teaching of BcgI and its recognition and cleavage patterns does not cure the inadequacies of Bensimon in teaching the methods of claims 90 and 99" and submit that "the steps of (a) identifying by determining nucleotide sequence of pieces of test eukaryotic cell genome, (b) enumerating the pieces within windows, and (c) comparing the number of pieces within a window of the test cell to the number determined similarly for a reference eukaryotic cell, are not taught by either Bensimon or Kong". Thus, Applicants argue that "even combining the two teachings, the subject matter of claims 96 and 108 is not taught". Furthermore, Applicants argue that the reference teachings

of cloning and probing procedures do not have a relationship to the claimed methods of identifying, enumerating, and comparing.

Applicants arguments have been fully considered but are not persuasive for reasons of record and presented herein. Specifically, Applicants argument that Bensimon et al fails to teach the method of the base claims is not persuasive because Applicants argument that Bensimon et al fails to teach "enumerating" because the "plain meaning of enumerating is counting" and that "determining the sum of sizes of objects is not the same as counting the number of objects" is not persuasive because the term “enumerating” can be read as “counting” or “listing” and clearly in order to determine the sum of sizes of objects both “counting” and “listing” would inherently be employed. In addition, although clearly the “probes” are not themselves the pieces of the genome, the probes are the identifiers of the pieces of the genome that are being analyzed.

In addition, Bensimon et al teach that any of several known molecular techniques can be used to assign a coding sequence to one or more of the clones selected in the preceding steps (see paragraphs 0027-0031 and 0152, for example), which meets the limitation of identifying pieces of the genome of a test eukaryotic cell by determining nucleotide sequence of said pieces.

In view of the foregoing, the method of 96 and 108, as a whole, would have been obvious to one of ordinary skill in the art at the time the invention was made. Therefore, the claims are properly rejected under 35 USC *§103(a).*

Conclusion

No claims are allowed.

THIS ACTION IS MADE FINAL. Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to CATHERINE HIBBERT whose telephone number is (571)270-3053. The examiner can normally be reached on M-F 8AM-5PM, EST.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Christopher Low can be reached on 571-272-0951. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only.

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Catherine Hibbert, Ph.D.

/ Christopher S. F. Low /
Supervisory Patent Examiner, Art Unit 1639